

Rec'd PCT/PTO 03 MAR 2006

10/544093

SEQUENCE LISTING

<110> Yednock, Ted
Vasquez, Nicki
Bard, Frederique
Seubert, Peter A.

<120> ACTIVE IMMUNIZATION TO GENERATE ANTIBODIES TO SOLUBLE A-BETA FOR PREVENTION AND TREATMENT OF AMYLOIDOGENIC DISEASE

<130> 15270J-009820US

<140> US 10/544,093
<141> 2004-01-31

<150> WO PCT/US2004/002856
<151> 2004-01-31

<150> US 60/444,150
<151> 2003-02-01

<160> 27

<170> PatentIn version 3.2

<210> 1
<211> 42
<212> PRT
<213> Homo sapiens

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Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala
35 40

<210> 2
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Reversomer of A-beta 1-5

<400> 2

Arg Phe Glu Ala Asp
1 5

<210> 3
<211> 17
<212> PRT

<213> Artificial

<220>

<223> Artificial peptide derived from residues 323-339 of ovalbumin.

<400> 3

Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly
1 5 10 15

Arg

<210> 4

<211> 16

<212> PRT

<213> Plasmodium sp.

<400> 4

Glu Lys Lys Ile Ala Lys Met Glu Lys Ala Ser Ser Val Phe Asn Val
1 5 10 15

<210> 5

<211> 10

<212> PRT

<213> Hepatitis B virus

<400> 5

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
1 5 10

<210> 6

<211> 19

<212> PRT

<213> Artificial

<220>

<223> Heat Shock Protein 65 fragment

<400> 6

Asp Gln Ser Ile Gly Asp Leu Ile Ala Glu Ala Met Asp Lys Val Gly
1 5 10 15

Asn Glu Gly

<210> 7

<211> 14

<212> PRT

<213> Artificial

<220>

<223> Bacille Calmette-Guerin fragment

<400> 7

Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu
1 5 10

<210> 8

<211> 15

<212> PRT

<213> Clostridium tetani

<400> 8

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 9

<211> 21

<212> PRT

<213> Clostridium tetani

<400> 9

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15

Ala Ser His Leu Glu
20

<210> 10

<211> 16

<212> PRT

<213> Human immunodeficiency virus

<400> 10

Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala
1 5 10 15

<210> 11

<211> 13

<212> PRT

<213> Artificial

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<223> PADRE peptide

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<223> X is cyclohexylalanine, tyrosine, or phenylalanine.

<400> 11

Ala Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
1 5 10

<210> 12
<211> 58
<212> PRT
<213> Artificial

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<223> Only a contiguous fragment of residues 1-43 are present.
Preferred fragments are 5-10 or 7-10 residues in length.

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Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Gln Tyr Ile Lys Ala
35 40 45

Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
50 55

<210> 13
<211> 64
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Preferred fragments are 5-10 or 7-10 residues in length.

<400> 13

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Phe Asn Asn Phe Thr
35 40 45

Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu
50 55 60

<210> 14
<211> 58
<212> PRT
<213> Artificial

<220>
<223> A-beta fragment-tetanus toxoid fusion protein

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<223> Only a contiguous fragment of residues 1-43 are present.
Preferred fragments are 5-10 or 7-10 residues in length.

<400> 14

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Gln Tyr Ile Lys Ala
35 40 45

Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
50 55

<210> 15
<211> 79
<212> PRT
<213> Artificial

<220>
<223> A-beta fragment tetanus-toxoid fusion protein

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Preferred fragments are 5-10 or 7-10 residues in length.

<400> 15

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1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Gln Tyr Ile Lys Ala
35 40 45

Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Phe Asn Asn Phe Thr Val
50 55 60

Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu
65 70 75

<210> 16
<211> 56
<212> PRT
<213> Artificial

<220>
<223> Padre-A-beta fragment fusion protein

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<223> X is cyclohexylalanine, tyrosine, or phenylalanine.

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<221> MISC_FEATURE
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<223> Only a contiguous fragment of residues 14-56 are present.
Preferred fragments are 5-10 or 7-10 residues in length.

<400> 16

Ala Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala Ala Asp Ala Glu
1 5 10 15

Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe
20 25 30

Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met
35 40 45

Val Gly Gly Val Val Ile Ala Thr
50 55

<210> 17
<211> 142
<212> PRT
<213> Artificial

<220>
 <223> A-beta-A-beta-A-beta-Padre fusion protein

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 <223> Only a contiguous fragment of residues 1-43 are present.
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<220>
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 <223> Only a contiguous fragment of residues 44-86 are present.
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<220>
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 <222> (87)..(129)
 <223> Only a contiguous fragment of residues 87-129 are present.
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 <222> (132)..(132)
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<400> 17

Asp	Ala	Glu	Phe	Arg	His	Asp	Ser	Gly	Tyr	Glu	Val	His	His	Gln	Lys	
1						5				10				15		

Leu	Val	Phe	Phe	Ala	Glu	Asp	Val	Gly	Ser	Asn	Lys	Gly	Ala	Ile	Ile
							20		25				30		

Gly	Leu	Met	Val	Gly	Gly	Val	Val	Ile	Ala	Thr	Asp	Ala	Glu	Phe	Arg
					35		40					45			

His	Asp	Ser	Gly	Tyr	Glu	Val	His	His	Gln	Lys	Leu	Val	Phe	Phe	Ala
					50		55			60			.		

Glu	Asp	Val	Gly	Ser	Asn	Lys	Gly	Ala	Ile	Ile	Gly	Leu	Met	Val	Gly
					65		70			75			80		

Gly	Val	Val	Ile	Ala	Thr	Asp	Ala	Glu	Phe	Arg	His	Asp	Ser	Gly	Tyr
						85		90				95			

Glu	Val	His	His	Gln	Lys	Leu	Val	Phe	Phe	Ala	Glu	Asp	Val	Gly	Ser
					100		105				110				

Asn	Lys	Gly	Ala	Ile	Ile	Gly	Leu	Met	Val	Gly	Gly	Val	Val	Ile	Ala
					115		120			125					

Thr Ala Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
130 135 140

<210> 18
<211> 185
<212> PRT
<213> Artificial

<220>
<223> Fusion protein

<220>
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<223> X is cyclohexylalanine, tyrosine, or phenylalanine.

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Preferred fragments are 5-10 or 7-10 residues in length.

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Preferred fragments are 5-10 or 7-10 residues in length.

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Preferred fragments are 5-10 or 7-10 residues in length.

<400> 18

Ala Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala Asp Ala Glu
1 5 10 15

Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe
20 25 30

Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met
35 40 45

Val Gly Gly Val Val Ile Ala Thr Asp Ala Glu Phe Arg His Asp Ser
50 55 60

Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val

65 70 75 80

Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val
85 90 95

Ile Ala Thr Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His
100 105 110

His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly
115 120 125

Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Asp Ala
130 135 140

Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val
145 150 155 160

Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu
165 170 175

Met Val Gly Gly Val Val Ile Ala Thr
180 185

<210> 19
<211> 56
<212> PRT
<213> Artificial

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<223> Fusion protein

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<223> Only a contiguous fragment of residues 1-43 are present.
Preferred fragments are 5-10 or 7-10 residues in length.

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<221> MISC_FEATURE
<222> (46)..(46)
<223> X is cyclohexylalanine, tyrosine, or phenylalanine.

<400> 19

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Ala Lys Xaa Val Ala
35 40 45

Ala Trp Thr Leu Lys Ala Ala Ala
50 55

<210> 20
<211> 60
<212> PRT
<213> Artificial

<220>
<223> Fusion protein

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Preferred fragments are 5-10 or 7-10 residues in length.

<400> 20

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1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Ile Ser Gln Ala Val
35 40 45

His Ala Ala His Ala Glu Ile Asn Glu Ala Gly Arg
50 55 60

<210> 21
<211> 142
<212> PRT

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Preferred fragments are 5-10 or 7-10 residues in length.

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Preferred fragments are 5-10 or 7-10 residues in length.

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Preferred fragments are 5-10 or 7-10 residues in length.

<400> 21

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr Asp Ala Glu
1 5 10 15

Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe
20 25 30

Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met
35 40 45

Val Gly Gly Val Val Ile Ala Thr Asp Ala Glu Phe Arg His Asp Ser
50 55 60

Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val
65 70 75 80

Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val
85 90 95

Ile Ala Thr Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His
100 105 110

His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly
115 120 125

Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr
130 135 140

<210> 22

<211> 99

<212> PRT

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<223> Only a contiguous fragment of residues 1-43 are present.
Preferred fragments are 5-10 or 7-10 residues in length.

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Preferred fragments are 5-10 or 7-10 residues in length.

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Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Val Val Ile Ala Thr Pro Lys Tyr Val Lys
35 40 45

Gln Asn Thr Leu Lys Leu Ala Thr Asp Ala Glu Phe Arg His Asp Ser
50 55 60

Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val
65 70 75 80

Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val
85 90 95

Ile Ala Thr

<210> 23
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Preferred fragments are 5-10 or 7-10 residues in length.

<220>
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<223> Only a contiguous fragment of residues 44-86 are present.
Preferred fragments are 5-10 or 7-10 residues in length.

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<221> MISC_FEATURE

<222> (87)..(129)
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Preferred fragments are 5-10 or 7-10 residues in length.

<400> 23

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1 5 10 15

.
Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Asp Ala Glu Phe Arg
35 40 45

His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe Ala
50 55 60

Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val Gly
65 70 75 80

Gly Val Val Ile Ala Thr Asp Ala Glu Phe Arg His Asp Ser Gly Tyr
85 90 95

Glu Val His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser
100 105 110

Asn Lys Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala
115 120 125

Thr Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
130 135 140

<210> 24
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<212> PRT
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<223> Fusion protein

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Preferred fragments are 5-10 or 7-10 residues in length.

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Preferred fragments are 5-10 or 7-10 residues in length.

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1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Asp Ala Glu Phe Arg
35 40 45

His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe Ala
50 55 60

Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val Gly
65 70 75 80

Gly Val Val Ile Ala Thr Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys
85 90 95

Leu Ala Thr

<210> 25
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Preferred fragments are 5-10 or 7-10 residues in length.

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<221> MISC_FEATURE
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<223> Only a contiguous fragment of residues 238-280 are present.
Preferred fragments are 5-10 or 7-10 residues in length.

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1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Pro Lys Tyr Val Lys
35 40 45

Gln Asn Thr Leu Lys Leu Ala Thr Glu Lys Lys Ile Ala Lys Met Glu
50 55 60

Lys Ala Ser Ser Val Phe Asn Val Gln Tyr Ile Lys Ala Asn Ser Lys
65 70 75 80

Phe Ile Gly Ile Thr Glu Leu Phe Asn Asn Phe Thr Val Ser Phe Trp
85 90 95

Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Asp Ala Glu Phe
100 105 110

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
115 120 125

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
130 135 140

Gly Gly Val Val Ile Ala Thr Asp Ala Glu Phe Arg His Asp Ser Gly
145 150 155 160

Tyr Glu Val His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly
165 170 175

Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile
180 185 190

Ala Thr Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His

195

200

205

Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala
210 215 220

Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Asp Ala Glu
225 230 235 240

Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe
245 250 255

Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met
260 265 270

Val Gly Gly Val Val Ile Ala Thr Gln Tyr Ile Lys Ala Asn Ser Lys
275 280 285

Phe Ile Gly Ile Thr Glu Leu Phe Asn Asn Phe Thr Val Ser Phe Trp
290 295 300

Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu
305 310 315

<210> 26
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Preferred fragments are 5-10 or 7-10 residues in length.

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Preferred fragments are 5-10 or 7-10 residues in length.

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<223> Only a contiguous fragment of residues 161-203 are present.
Preferred fragments are 5-10 or 7-10 residues in length.

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Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys

1

5

10

15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Gln Tyr Ile Lys Ala
35 40 45

Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Cys Phe Asn Asn Phe Thr
50 55 60

Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu
65 70 75 80

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
85 90 95

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
100 105 110

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Gln Tyr Ile Lys Ala
115 120 125

Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Cys Phe Asn Asn Phe Thr
130 135 140

Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu Glu
145 150 155 160

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
165 170 175

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
180 185 190

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr
195 200

<210> 27
<211> 58
<212> PRT
<213> Artificial

<220>
<223> Fusion protein

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<221> MISC_FEATURE
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<223> Only a contiguous fragment of residues 1-43 are present.
Preferred fragments are 5-10 or 7-10 residues in length.

<400> 27

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Gln Tyr Ile Lys Ala
35 40 45

Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
50 55